

Figure 1

Map of Human CD20/IgE-Receptor Like cDNA (SEQ ID NO: 1) and  
Amino Acid Sequence (SEQ ID NO: 2)

5

(Agp-96614-a1)  
(CD20RP2)

1	TTCCAGTGCTCCAGGCAGCCTCAGCACAAAGAAAAGAACATGGTCTAGACTGAAGTACCAA	60
61	CTAAATCATCTCCTTCAAATTATCACCGACACCACATGGATTCAAGCACCGCACACAG	120
1	M D S S T A H S	8
121	TCCGGTGTCTGGTATTCCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACT	180
9	P V F L V F P P E I T A S E Y E S T E L	28
181	TTCAGGCCACGACCTTCAACTCAAAGCCCCGGCAAAAAATTATGGCTAGAAAAATGAA	240
29	S A T T F S T Q S P L Q K L F A R K M K	48
241	AATCTTAGGGACTATCCAGATCCTGTTGGATTATGACCTTTCTTTGGAGTTATCTT	300
49	I L G T I Q I L F G I M T F S F G V I F	68
301	CCTTTCACTTTGTTAAACCATATCCAAGGTTCCCTTATATTCTTCAGGATATCC	360
69	L F T L L K P Y P R F P F I F L S G Y P	88
361	ATTCTGGGGCTCTGTTGTTCATTAATTCTGGAGCCTCCTAATTGCAGTGAAAAGAAA	420
89	F W G S V L F I N S G A F L I A V K R K	108
421	AACCACAGAAACTCTGATAATATTGAGCCGAATAATGAATTTCTTAGTGCCTGGAGC	480
109	T T E T L I I L S R I M N F L S A L G A	128
481	AATAGCTGGAATCATTCTCCTCACATTGGTTCATCCTAGATCAAAACTACATTGTGG	540
129	I A G I I L L T F G F I L D Q N Y I C G	148
541	TTATTCTCACCAAAATAGTCAGTGTAAGGCTGTTACTGTCCTGTTCTGGGAATTTGAT	600
149	Y S H Q N S Q C K A V T V L F L G I L I	168
601	TACATTGATGACTTTCAGCATTATTGAATTATTCAATTCTCTGCCCTTCTCAATTGGG	660
169	T L M T F S I I E L F I S L P F S I L G	188
661	GTGCCACTCAGAGGATTGTGATTGTGAACAATGTTGTTGACTAGCACTGTGAGAATAAG	720
189	C H S E D C D C E Q C C *	201
721	ATGTGTTAAATCTCAAAAAAAAAAAAAAAA 760	

Figure 2

Map of Human CD20/IgE-receptor Like cDNA (SEQ ID NO: 3) and  
Amino Acid Sequence (SEQ ID NO: 4)  
5 (Agp-69406-a1)  
10 (CD20RP1)

1	GGCAGGAACAGCCAGTGGGAGGTTCCAGCTGAGCGCTCCCCAGAGGTGAGCTGATCCCCA	60
61	GCCACAGCACACAGGACCAGGCTGCGAGAACAGCATCATCAGCATCATGCTATTACAATC	120
1	M L L Q S	5
121	CAAACCATGGGGTTCTCACAGTTACACCAAAGGGCATCACTATCCCTCAAAGAGA	180
6	Q T M G V S H S F T P K G I T I P Q R E	25
181	GAAACCTGGACACATGTACCAAAACGAAGATTACCTGCAGAACGGCTGCCAACAGAAC	240
26	K P G H M Y Q N E D Y L Q N G L P T E T	45
15	241 CACCGTTCTGGACTGTCCAGATCCTGTGTTGCCTGTTGATTCAGTCTGGGGGCCAT	300
	46 T V L G T V Q I L C C L L I S S S L G A I	65
301	CTTGGTTTGCTCCCTACCCCTCCACTTCATCCAGCAATTCCACCACTTGATGTC	360
66	L V F A P Y P S H F N P A I S T T L M S	85
20	361 TGGGTACCCATTAGGAGCTCTGTGTTGGCATTACTGGATCCCTCTCAATTATCTC	420
	86 G Y P F L G A L C F G I T G S L S I I S	105
421	TGGAAAACAATCAACTAAGCCCTTGACCTGAGCAGCTGACCTCAAATGCAGTGAGTT	480
106	G K Q S T K P F D L S S L T S N A V S S	125
481	TGTTACTGCAGGAGCAGGCCTTCTGCTGACAGCATGGTAGCCCTGAGGACTGC	540
126	V T A G A G L F L L A D S M V A L R T A	145
25	541 CTCTCAACATTGTGGCTCAGAAATGGATTATCTATCCTCATTGCCTTATTGGAGTACTA	600
	146 S Q H C G S E M D Y L S S L P Y S E Y Y	165
601	TTATCCAATATATGAAATCAAAGATTGTCTCTGACCAGTGTCAAGTTAACAGGTGTCC	660
166	Y P I Y E I K D C L L T S V S L T G V L	185
30	661 AGTGGTGATGCTCATCTTCACTGTGCTGGAGCTCTTATTAGCTGCATACAGTTCTGTCTT	720
	186 V V M L I F T V L E L L A A Y S S V F	205
721	TTGGTGGAAACAGCTCTACTCCAACAACCTGGAGTCATTCTCGACCCAGTCACA	780
206	W W K Q L Y S N N P G S S F S S T Q S Q	225
781	AGATCATATCCAACAGGTCAAAAGAGTTCTCACGGTCTGGATATAAGTAACCTTGG	840
226	D H I Q Q V K K S S S R S W I *	241
35	841 CCTCAGAGGAAGGAAAAGCAACTAACACTCATGGTCAAGTGTGATTAGACTTTCTGAA	900
901	ATCTCTGCCATTAGATACTGTGAAACAAACTAAAAAAAAAGCTTTGTTTGTATT	960
961	GAAAAAAAAAAAAAAA 982	

Figure 3

HTM4	M --- ASH-E	VDN---AELG	SASA-----	HSTPGSETOP	EEL-NI---S	32
11 GERB	PHOTYSRHR	PEE---STFS	ARMITNGME	GAMPGAGPQI	POLGNM---A	44
HURP4	M --- TSOVY	PNE---TIIY	LPS-----	MN IF SRAIK	PEI-----P	29
69406	M --- LLQSQ	TNG---V95	FTP-----	KG TI PORK	PG-----H	29
1 qERbeta	MD---TE SNR	RAN---LAP	GEPSSVPVF	EVEI SPRIV	SSGRLL---K	40
96614	M --- DS STA	HSP---VFLV	FPP-----	-ETI TASEYES	TEL-SA---T	21
HTPEF86	MNSMISAVPV	ANSILVVPH	NGV PV TPGI M	SWPL VFNDR	POV/HLV RGP	50
KCD20	HTTPRSV---	-----N	GTF PAEP-MK	GP1 AMRSGRK	P---LFR FM	34
HTMSF5	HTDTGQA---	-----	-----	ROGL-----	-----	12
HTAL6	HDYQDAA	-----	-----	ROI GH-----	-----	12
Conz enz w	M .....	.....	.....	.....	.....	50
HTM4	WV HPI --- NGS	PD-YOKAHLR	VLGAQD LNA	AM LALGIVL	GSL QYPVHFO	79
11 GERB	WV HGMWKGSL	QEFKL KSEPK	VLGVVQ LTA	LMLSLMGTIM	MOMA-SNY VG	93
HURP4	THQG---DSL	KG-ML HAB K	VI GTI Q LOG	MYLSLGJL	ASAFSFNFT	76
69406	MIGRE---DLV	OH-G PTETT	VLGTVQ LOC	LLI SSSLGAI	VFAPVPSHN	76
1 qERbeta	SASSPLHWT	LT-VL KYDDE	FLGTVQ LTA	M OLOFGKWW	CSQLDI SHF	89
96614	TF STG---SPL	QK-LF ARMYK	LLGTI Q LFG	IMTFSQHIF	LFTL-LHPYV	77
HTPEF86	PSLVSNNGQ	PVOKALKEGK	TLGAQJ I G	LAH GLOSSM	ATVL-V EYL	99
KCD20	SSLVQ---PTQ	TF-F MHESK	TLGAVQ MNG	LFI ALQELL	M-P AG YA	78
HTMSF5	-SLIT-----	-----L---	OFVO-WANA	LLVLPNGE--	-TSW-TH-N	41
HTAL6	-SLVQ-----	-----L-	ALLC-SAN	LLYFPNGE--	-TKV-AE-Z-N	41
Conz enz w	.....	.....E.	LG. I QL..	L...G..	.....	100
HTM4	KHFFFFFTFYT	GPVI WGAWTF	CSSGTL SWVVA	GI KP-----	-----T-	114
11 GERB	SN---PI SVV	GTII WGSVMT	II SGSLVAA	GI RT-----	-----T-	124
HURP4	QV-TSTL LNS	AIVPFI GRFTT	II SGSLVAT	EKRL-----	-----T-	110
69406	PA---STTL LMS	GIPFL GALOF	GI TGSLV I S	GROS-----	-----T-	110
1 qERbeta	GD-I FSSFKA	GIPFWGIAFF	SI SGSLV I S	ERPN-----	-----A-	123
96614	Pa---FPI FLS	GIPFWGSLLF	I NSGFLV I W	KPKT-----	-----T-	110
HTPEF86	SI SYVGGF-	PF-W GLWV	II SGSLVPA	ENOP-----	-----VS-	131
KCD20	PI OTVWW-	PL-W GSIM	II SGSLLAAT	EKNS-----	-----Pr	109
HTMSF5	HL SLOWLNG	GP-I GGSLM	LOGI AW PA	GGHDGAGC	OQN---PC	**
HTAL6	HL SRVWHTS	G-YGGSLM	LLPAPV IT GL	EODDOO---QZ	QGHENCGKRC	**
Conz enz w	.....	GY...G..F	ISG LS...	.....	.....	150
HTM4	-----	-----RIV	I ONSF QHITA	SATI ALVFTA	FLSLN AVNI	147
11 GERB	-----	-----KZL	VRGSL QHILT	SSHLASGLI	I NTFSL FV-	152
HURP4	-----	-----MLL	VHSL VQSL L	SALSALVGR	I LSXKQAF LN	143
69406	-----	-----MPF	DLSL TSNAV	SSTAGKGLF	LLADSMALR	143
1 qERbeta	-----	-----TYL	VRGSL QHITA	SS AGGTGT	I LI I HL KSL	156
96614	-----	-----ETL	I IL SRIM PMFL	SALGH AGII	LLT FGF ILDQ	143
HTPEF86	-----	-----YOL	LSGSL QLNVY	SAI CSANGW	LTI TDL--S	161
KCD20	-----	-----KOL	VIRGHMIMSL	SFAAI SGH	LSI MD LH K	142
HTMSF5	PMIERSW SSA	FGI LGI YOL	SVSGAGLRG	PROLMN GEM	GHFIE---D	130
HTAL6	AMLSVIAL	I G AGSYI OY	I VAI ALGAEQ	FLODSLGM	NYT FA ---S	134
Conz enz w	.....	-----L	SLG N...	S...A.G.	.....	200
HTM4	OSLRSOHSSS	E --- SPIDC	NWMSG---I	SN-----	-GMWSL-LI	179
11 GERB	-STH---H-	-P-YC	NNV GH---S	NNOHGTMISL	MG DGM---LL	190
HURP4	PASLQCLDK	N-N PTRSY	STY YHDSL YT	TDDY AKAS.	AGT LSLM LI	191
69406	TASOMHGSSEM	D-YVSSLFYS	ETVYV-1 YEI	KDGL TSV SL	TG/LVVM LI	190
1 qERbeta	AVI H-----	---I HSDF	KFF---E	TKQFMASF S	TEI VUHM LF	187
96614	WV-----	---C	GYSHR---N	SOCKA-----	VTV LFLG I L	167
HTPEF86	I PH-----	---PV	DVY-----	---P---Y	ANGSTNP G M	183
KCD20	I SHFLKIMESL	NFI RAHT PW	N YNODPANP	SENKPST QV	OYSI OSLF LG	192
HTMSF5	TAG-----	AVILLNRUW	ROE-----	---AP---	PRV VEWN VT	157
HTAL6	TEG-----	QHLLDTSTWS	ECT-----	---EP---	KHI VEWN VS	161
Conz enz w	.....	....Y.	....	....L.	....	250
HTM4	LTLLLELCVTI	STI AM-----	---WON-	---ANON-S	-----	203
11 GERB	LSVLEFCI AV	SLSAF-----	---GOK-	---VL OCT-P	GGV LLI UPSH	224
HURP4	OTLLEFCI CLAV	LTAWL-----	---PRW-	---GAYSDFP	GSV LFL RHY	226
69406	FTVLELLAAR	YSSW-----	---WAK-	---OL YSNHP	GSST SSTS-	224
1 qERbeta	LT1 LGLGSAW	SLTIC-----	---GAG-	---EE LKGMK	VPE DRW EEL	222
96614	ITLMFTSII	LFISL-----	---PFS-	---I LGOH-	-----	190
HTPEF86	I SGULLVFL	LEFB-----	---ACAS	SHFGQLY CO	---QSEW	217
KCD20	I LSVMI FAF	FEGLVIAV Y	ENEWKFRCSR	PSHN VLL SA	EEKREQT EI	242
HTMSF5	LF SLVVAASC	LEI VL-----	---C--	---GI QLV--	-----NATI	182
HTAL6	LFS LLLALGG	I EFIL-----	---C--	---LI QVI --	-----NSVL	186
Conz enz w	...L.L...	.....	C.-	.....	.....	200
HTM4	-- REEI SSP-	P-N-----	--SV-----	-----	-----	214
11 GERB	SHMETASP	PLN-----	--EV-----	-----	-----	239
HURP4	I GNSGM659M	THD-----	--QYV ELLT	S-----	-----	248
69406	-QDH QDVKC	SSS-----	--RSW-----	-----	-----	240
1 qERbeta	M YSATYSEL	EDP-----	--GEMSPPI D	L-----	-----	244
96614	-- SEDOCCE-	--O-	--CO-----	-----	-----	200
HTPEF86	-- SW YPHN Y	ARNP-----	--V T-----	---PIP	UTSPPSVSE	245
KCD20	KEEVNGLET	SSQPKHE ED	EII PI GEEE	EETETNFPBP	PODGESP E	292
HTMSF5	-- GFO---	-----	-----	-----	-- GDCRKK	193
HTAL6	-- GG D-	-----	-----	-----	-- GFCOSH	197
Conz enz w	-----	-----	-----	-----	-----	350
HTM4	-----	-----	-----	-----	-----	214
11 GERB	-----	-----	-----	-----	-----	239
HURP4	-----	-----	-----	-----	-----	248
69406	-----	-----	-----	-----	-----	240
1 qERbeta	-----	-----	-----	-----	-----	244
96614	-----	-----	-----	-----	-----	200
HTPEF86	I QANK	-----	-----	-----	-----	250
KCD20	NDSSP	-----	-----	-----	-----	297
HTMSF5	DT-PH	-----	-----	-----	-----	197
HTAL6	QQYDC	-----	-----	-----	-----	202
Conz enz w	-----	-----	-----	-----	-----	355